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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/09/090,672A**

DATE: 01/05/2000  
 TIME: 04:16:25

INPUT SET: S34368.raw

**This Raw Listing contains the General  
 Information Section and those Sequences  
 containing ERRORS.**

Does Not Comply  
 Corrected Diskette Needed

## SEQUENCE LISTING

1  
 2  
 3 (1) General Information:  
 4 (i) APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,  
 5 Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,  
 6 Shigemasa; Takei, Masami  
 7 (ii) TITLE OF INVENTION: IgA Nephropathy-Related Genes  
 8 (iii) NUMBER OF SEQUENCES: 111  
 9 (iv) CORRESPONDENCE ADDRESS:  
 10 (A) ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto  
 11 (B) STREET: 30 Rockefeller Plaza  
 12 (C) CITY: New York  
 13 (D) STATE: New York  
 14 (E) ZIP: 10112-3801  
 15 (v) COMPUTER READABLE FORM:  
 16 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
 17 (B) COMPUTER: Compac PC  
 18 (C) OPERATING SYSTEM: Windows 95  
 19 (D) SOFTWARE: WordPerfect 8.0  
 20 (vi) CURRENT APPLICATION DATA:  
 21 (A) APPLICATION NUMBER: 09/090,672  
 22 (B) FILING DATE: 04-JUNE-1998  
 23 (C) CLASSIFICATION: 435  
 24 (vii) PRIOR APPLICATION DATA:  
 25 (A) APPLICATION NUMBER: PCT/JP97/04468  
 26 (B) FILING DATE: 05-DEC-1997  
 27 (A) APPLICATION NUMBER: JP-8-325763  
 28 (B) FILING DATE: 05-DEC-1996  
 29 (viii) ATTORNEY/AGENT INFORMATION:  
 30 (A) NAME: Perry, Lawrence S.  
 31 (B) REGISTRATION NUMBER: 31865  
 32 (C) REFERENCE/DOCKET NUMBER: 766.21  
 33 (ix) TELECOMMUNICATION INFORMATION:  
 34 (A) TELEPHONE: (212) 218-2100  
 35 (B) TELEFAX: (212) 218-2200  
 36

## ERRORED SEQUENCES FOLLOW:

545 (2) INFORMATION FOR SEQ ID NO:8:  
 546 (i) SEQUENCE CHARACTERISTICS:  
 --> 547 (A) 278 base pairs

↓  
 LENGTH:

add the MANDATORY leading

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/090,672ADATE: 01/05/2000  
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548 (B) TYPE: nucleic acid  
549 (C) STRANDEDNESS: double  
550 (D) TOPOLOGY: linear  
551 (ii) MOLECULE TYPE: cDNA  
552 (vi) ORIGINAL SOURCE:  
553 (A) ORGANISM: human  
554 (G) CELL TYPE: leukocyte  
555 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
556 GAAGGAGAAT ATGAAGAGGT TAGAAAAGNT CNGGNTTCTG TTGGTGAAAT GAAGGATGAA 60  
557 GGGGAAGAGA CATTAAATTA TCCTGATACT ACCATTGACT TGTCTCACCT TCAACCCCAA 120  
558 AGGTCCATCC AGAAATTGGC TTCAAAGAG GAATCTTCTA ATTCTAGTGA CAGTAAATCA 180  
559 CAGAGCCGGA GACATTTGTC AGCCAAGGAA AGAAGGGAAA TGAAAAAGAA AAAACTTCCA 240  
560 AGTGACTCAG GAGATTTAGA AGCGTTAGAG GGAAAGGA 278  
561

1044 (2) INFORMATION FOR SEQ ID NO:36:  
1045 (i) SEQUENCE CHARACTERISTICS: 132 listed  
--> 1046 (A) LENGTH: 133 amino acids  
--> 1047 (B) SEQUENCE TYPE: amino acid  
1048 (D) TOPOLOGY: linear delete SEQUENCE - just use TYPE  
1049 (ii) MOLECULE TYPE: protein  
1050 (vi) ORIGINAL SOURCE:  
1051 (A) ORGANISM: human  
1052 (G) CELL TYPE: leukocyte  
1053 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:  
1054 Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr  
1055 1 5 10 15Pro Thr Ala  
1056 Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser  
1057 20 25 30  
1058 Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser  
1059 35 40 45  
1060 Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro  
1061 50 55 60  
1062 Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys  
1063 65 70 75 80  
1064 Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu  
1065 85 90 95  
1066 Ser Leu Glu Pro Ala Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys  
1067 100 105 110  
1068 Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe  
1069 115 120 125  
1070 Thr Arg Thr Asp Ile  
1071 130  
1072

1102 (2) INFORMATION FOR SEQ ID NO:38:  
1103 (i) SEQUENCE CHARACTERISTICS:  
--> 1104 (A) LENGTH: 128 amino acids  
--> 1105 delete (B) SEQUENCE TYPE: amino acid  
1106 (D) TOPOLOGY: linear  
1107 (ii) MOLECULE TYPE: protein  
1108 (vi) ORIGINAL SOURCE:  
1109 (A) ORGANISM: human

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/090,672A

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1110 (G) CELL TYPE: leukocyte  
1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:  
1112 Met Asp Ala Val Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly  
1113 1 5 10 15  
1114 Glu Lys Leu Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg  
1115 20 25 30  
1116 Asp Ser Glu Ser Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His  
1117 35 40 45  
1118 Gly Tyr Ile Tyr Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp  
1119 50 55 60  
1120 Ser Ala Glu Thr Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile  
1121 65 70 75 80  
1122 Lys Asn Leu Ile Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile  
1123 85 90 95  
1124 Pro Leu Gln Tyr Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln  
1125 100 105 110  
1126 Gly Thr Thr Gly Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro  
1127 115 120 125  
1128

1129 (2) INFORMATION FOR SEQ ID NO:39:  
--> 1130 (A) ~~IT~~ LENGTH: 305 base pairs  
--> 1131 (B) ~~IT~~ TYPE: nucleic acid  
--> 1132 (C) ~~IT~~ STRANDEDNESS: double  
--> 1133 (D) ~~IT~~ TOPOLOGY: linear  
--> 1134 (E) ~~IT~~ MOLECULE TYPE: cDNA  
1135 (vi) ~~IT~~ ORIGINAL SOURCE:  
1136 (A) ORGANISM: human  
1137 (G) CELL TYPE: leukocyte  
--> 1138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:  
--> 1139 TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGTTATGA GATTAAACCC ACNNNNNNNTT 60  
--> 1140 ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGATCTGG ATTTTGTCA TATGTGGAAT 120  
--> 1141 CATAATTTAA ACAAATCAA CTAAGATGAT CCAAGTTCCA CACAACTGCA CTTCAATATT 180  
--> 1142 CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCACAAGAT TCTGAGCTGT CGTAAAAAGC 240  
--> 1143 CTGGCTCGTG GTTCTATTT ATAGTG TACA CATGTTGGGT TATAATCACA AACCTGGAAC 300  
--> 1144 TCTGT 305  
1145

1427 (2) INFORMATION FOR SEQ ID NO:66:  
--> 1428 (i) (1) SEQUENCE CHARACTERISTICS:  
--> 1429 (A) LENGTH: 22 base pairs  
--> 1430 (B) TYPE: nucleic acid  
--> 1431 (C) STRANDEDNESS: single  
--> 1432 (D) TOPOLOGY: linear  
1433 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA  
--> 1434 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:  
1435 GCGTGGAATC AAATGGAGTG GC  
1436

# SEQUENCE VERIFICATION REPORT

## PATENT APPLICATION US/09/090,672A

 DATE: 01/05/2000  
 TIME: 04:16:26

INPUT SET: S34368.raw

Line	Error	Original Text
23	Wrong Classification	(C) CLASSIFICATION: 435
532	Entered (155) and Calc. Seq. Length (278) differ	(A) LENGTH: 155 base pairs
547	Unknown or Misplaced Identifier	(A) 278 base pairs
1046	Entered (133) and Calc. Seq. Length (131) differ	(A) LENGTH: 133 amino acids
1047	Unknown or Misplaced Identifier	(B) SEQUENCE TYPE: amino acid
1104	Entered (128) and Calc. Seq. Length (0) differ	(A) LENGTH: 128 amino acids
1105	Unknown or Misplaced Identifier	(B) SEQUENCE TYPE: amino acid
1130	Unknown or Misplaced Identifier	(i) LENGTH: 305 base pairs
1131	Unknown or Misplaced Identifier	(A) TYPE: nucleic acid
1132	Unknown or Misplaced Identifier	(B) STRANDEDNESS: double
1133	Unknown or Misplaced Identifier	(C) TOPOLOGY: linear
1134	Unknown or Misplaced Identifier	(D) MOLECULE TYPE: cDNA
1138	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACCTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACCTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACCTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACCTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACCTG TTTAGACTAG AATGT
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1144	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1419	Entered (24) and Calc. Seq. Length (22) differ	TCTGT
1428	Unknown or Misplaced Identifier	(A) LENGTH: 24 base pairs
1429	Unknown or Misplaced Identifier	(1) SEQUENCE CHARACTERISTICS:
1430	Unknown or Misplaced Identifier	(A) LENGTH: 22 base pairs
		(B) TYPE: nucleic acid

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/090,672A**DATE: 01/05/2000  
TIME: 04:16:27**INPUT SET: S34368.raw**

Line	Error	Original Text
1431	Unknown or Misplaced Identifier	(C) STRANDEDNESS: single
1432	Unknown or Misplaced Identifier	(D) TOPOLOGY: linear
1434	Wrong Or Missing Strandedness Value	(xi)SEQUENCE DESCRIPTION: SEQ ID NO:66:
1434	Wrong or Missing Sequence Topology	(xi)SEQUENCE DESCRIPTION: SEQ ID NO:66: